

FIG. 1A

Input file Fbh18903FL.seq; Output File 18903.trans
Sequence length 1983

CCTTTAGCCAATTCCGGCCGAGGCCCTCCCGCCAGTACTTGCTGGCAGGGATTAAAGACAGATATAAAGTGTGCTCACAC
 15
 ACTGTAGACACGGCTACC ATG CCA TCC ACA GTG TTG CCA TCC ACA GTG TTG CCA TCA CTC CTG 45
 M P S T V L P S T V L P S L L
 P T A G A G W S M R W I L C W S L T L C 35
 CCC ACA GCA GGA GCT GGC TGG AGC ATG AGG TGG ATT CTG TGC TGG AGC CTC ACC CTC TGC 105
 L M A Q T A L G A L H T K R P Q V V T K 55
 CTG ATG GCG CAG ACG GCC TTG GGT GCC TTG CAC ACC AAG AGG CCT CAA GTG GTC ACC AAA 165
 Y G T L Q G K Q M H V G K T P I Q V F L 75
 TAT GGA ACC CTG CAA GGA AAA CAG ATG CAT GTG GGG AAG ACA CCC ATC CAA GTG TTT TTA 225
 G V P F S R P P L G I L R F A P P E P P 95
 GGA GTC CCC TTC TCC AGA CCT CCT CTA GGT ATC CTC AGG TTT GCA CCT CCA GAA CCC CCG 285
 E P W K G I R D A T T Y P P G C L Q E S 115
 GAG CCC TGG AAA GGA ATC AGA GAT GCT ACC ACC TAC CCG CCT GGG TGC CTG CAG GAG TCC 345
 W G Q L A S M Y V S T R E R Y K W L R F 135
 TGG GGC CAG CTG GCC TCG ATG TAC GTC AGC ACC CGG GAA CGG TAC AAG TGG CTG CGC TTC 405
 S E D C L Y L N V Y A P A R A P G D P Q 155
 AGC GAG GAC TGT CTG TAC CTG AAC GTG TAC GCG CCG GCG CGC CCC GGG GAT CCC CAG 465
 L P V M V W F P G G A F I V G A A S S Y 175
 CTG CCA GTG ATG GTC TGG TTC CCG GGA GGC GCC TTC ATC GTG GGC GCT TCT TCG TAC 525

FIG. 1B

E	G	S	D	L	A	A	R	E	K	V	V	L	V	F	L	Q	H	R	L	195
GAG	GGC	TCT	GAC	TTG	GCC	GCC	CGC	GAG	AAA	GTG	GTG	CTG	GTG	TTT	CTG	CAG	CAC	AGG	CTC	585
G	I	F	G	F	L	S	T	D	D	S	H	A	R	G	N	W	G	L	L	215
GGC	ATC	TTC	GGC	TTC	CTG	AGC	ACG	GAC	GAC	AGC	CAC	CGC	CGC	GGG	AAC	TGG	GGG	CTG	CTG	645
D	Q	M	A	A	L	R	W	V	Q	E	N	I	A	A	F	G	G	D	P	235
GAC	CAG	ATG	CGG	GCT	CTG	CGC	TGG	GTG	CAG	GAG	AAC	ATC	GCA	GCC	TTC	GGG	GGA	GAC	CCA	705
G	N	V	T	L	F	G	Q	S	A	G	A	M	S	I	S	G	L	M	M	255
GGA	AAT	GTG	ACC	CTG	TTC	GGC	CAG	TCG	GCG	GGG	GCC	ATG	AGC	ATC	TCA	GGA	CTG	ATG	ATG	765
S	P	L	A	S	G	L	F	H	R	A	I	S	Q	S	G	T	A	L	F	275
TCA	CCC	CTA	GCC	TCG	GGT	CTC	TTC	CAT	CGG	GCC	ATT	TCC	CAG	AGT	GGC	ACC	GCG	TTA	TTC	825
R	L	F	I	T	S	N	P	L	K	V	A	K	K	V	A	H	L	A	G	295
AGA	CTT	TTC	ATC	ACT	AGT	AAC	CCA	CTG	AAA	GTG	GCC	AAG	AAG	GTT	GCC	CAC	CTG	GCT	GGA	885
C	N	H	N	S	T	Q	I	L	V	N	C	L	R	A	L	S	G	T	K	315
TGC	AAC	CAC	AAC	AGC	ACA	CAG	ATC	CTG	GTA	AAC	TGC	CTG	AGG	GCA	CTA	TCA	GGG	ACC	AAG	945
V	M	R	V	S	N	K	M	R	F	L	Q	L	N	F	Q	R	D	P	E	335
GTG	ATG	CGT	GTG	TCC	AAC	AAG	ATG	AGA	TTC	CTC	CAA	CTG	AAC	TTC	CAG	AGA	GAC	CCG	GAA	1005
E	I	I	W	S	M	S	P	V	V	D	G	V	V	I	P	D	D	P	L	355
GAG	ATT	ATC	TGG	TCC	ATG	AGC	CCT	GTG	GTG	GAT	GGT	GTG	GTG	ATC	CCA	GAT	GAC	CCT	TTG	1065
V	L	L	T	Q	G	K	V	S	S	V	P	Y	L	L	G	V	N	N	L	375
GTG	CTC	CTG	ACC	CAG	GGG	AAG	GTT	TCA	TCT	GTG	CCC	TAC	CTT	CTA	GGT	GTC	AAC	AAC	CTG	1125
E	F	N	W	L	L	P	Y	I	M	K	F	P	L	N	R	Q	A	M	R	395
GAA	TTC	AAT	TGG	CTC	TTG	CCT	TAT	ATC	ATG	AAG	TTC	CCG	CTA	AAC	CGG	CAG	GCG	ATG	AGA	1185

FIG. 1C

K E T I T K M L W S T R T L L N I T K E 415
 AAG GAA ACC ATC ACT AAG ATG CTC TGG AGT ACC CGC ACC CTG TTG AAT ATC ACC AAG GAG 1245

 Q V P L V V E E Y L D N V N E H D W K M 435
 CAG GTA CCA CTT GTG GTG GAG GAG TAC CTG GAC AAT GTC AAT GAG CAT GAC TGG AAG ATG 1305

 L R N R M M D I V Q D A T F V Y A T L Q 455
 CTA CGA AAC CGT ATG ATG GAC ATA GTT CAA GAT GCC ACT TTC GTG TAT GCC ACA CTG CAG 1365

 T A H Y H R D A G L P V Y L Y E F E H H 475
 ACT GCT CAC TAC CAC CGA GAT GCC GGC CTC CCT GTC TAC CTG TAT GAA TTT GAG CAC CAC 1425

 A R G I I V K P R T D G A D H G D E M Y 495
 GCT CGT GGA ATA ATC GTC AAA CCC CGC ACT GAT GGG GCA GAC CAT GGG GAT GAG ATG TAC 1485

 F L F G G P F A T G L S M G K E K A L S 515
 TTC CTC TTT GGG GGC CCC TTC GCC ACA GGC CTT TCC ATG GGT AAG GAG AAG GCA CTT AGC 1545

 L Q M M K Y W A N F A R T G N P N D G N 535
 CTC CAG ATG ATG AAA TAC TGG GCC AAC TTT GCC CGC ACA GGA AAC CCC AAT GAT GGG AAT 1605

 L P C W P R Y N K D E K Y L Q L D F T T 555
 CTG CCC TGC TGG CCA CGC TAC AAC AAG GAT GAA AAG TAC CTG CAG CTG GAT TTT ACC ACA 1665

 R V G M K L K E K M A F W M S L Y Q S 575
 AGA GTG GGC ATG AAG CTC AAG GAG AAG AAG ATG GCT TTT TGG ATG AGT CTG TAC CAG TCT 1725

 Q R P E K Q R Q F * 585
 CAA AGA CCT GAG AAG CAG AGG CAA TTC TAA 1755

GGGTGGCTATGCAGGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGACTAGCCATGGACATACC

TGGGGACAAGAGTTCTACCCCAAGGGCGAATTCGTTTAAACCTGCAGGACTAG

FIG. 2

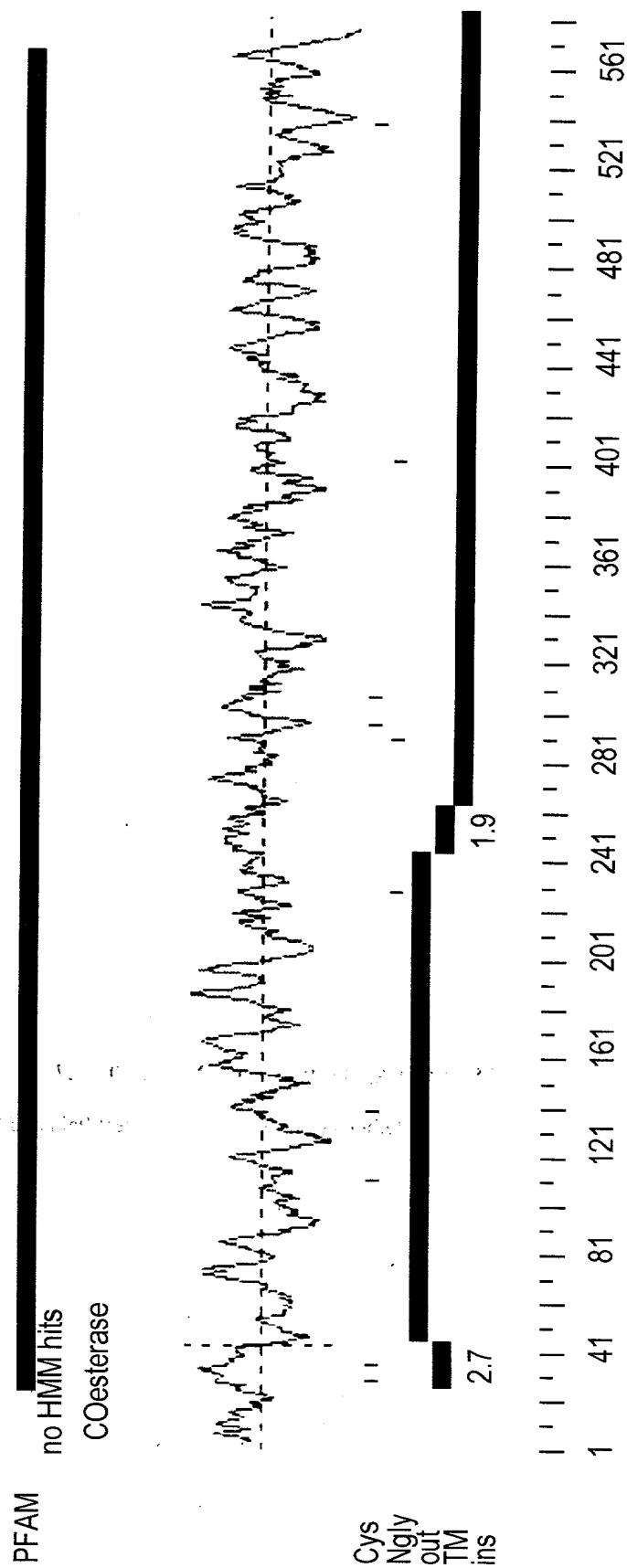


FIG. 3A

Protein Family / Domain Matches, HMMer version 2

Searching for complete domains in PFAM
hmpfam - search a single seq against HMM database
HMMER 2.1.1 (Dec 1998)
Copyright (C) 1992-1998 Washington University School of Medicine
HMMER is freely distributed under the GNU General Public License (GPL).

HMM file: /prod/ddm/seganal/pfam6.4/pfam
Sequence file: /prod/ddm/wspace/orfanel/oa-script.6214.seq

Query: Fbh18903FL

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
COesterase	Carboxylesterase	558.6	4.1e-164	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
COesterase	1/1	25	569	1	612	558.6	4.1e-164

Alignments of top-scoring domains:

COesterase: domain 1 of 1, from 25 to 569: score 558.6, E = 4.1e-164

*->mvlllllfllllllllaavlaaakaspdp1lVatnnVlcGkvrGvnek
+l+ +L 1 1 ++ +l+a+++ ++ V t++ G++ G++

18903 25 RWILCWSLTLCMAQTALGALHT---KRPQVVTKY---GTLQKQMH 65

tdngeqsvysFlGIPYAepFVGnLRFkaPqPYkepWsdvldatkyppsCl
+ ++ +FlG+P+ PP+G LRF +P+P +epW++++dat+ypp Cl

18903 66 VGKT--PIQVFLGVFSPRPPLGILRFAPPEP-PEPWKIGIRDATYPGCL 112

FIG. 3B

QdddfgfsldLKvalkmlslgwnklvg....lklsEDCLYLNvYtPknt
 Q + +g+ 1 +++ ++ + 1 +sEDCLYLNvY P+ +
 18903 113 Q-ESWGQ-----LASMVSTRerykwlRFSEDCLYLNvYAPARA 150

 kpnsklPVmVwIhGGGFmfGsgshslplslYdgeslaregnVivVsiNYRL
 + + +lPVmVw +GG+F +G++ s+Y g+ la++++V++V ++ RL
 18903 151 PGDPQLPVMVWFPGGAFIVGAA-----SSYEGSDLAAREKVVLVFLQHRL 195

 GplGFLstgddklpgsGNyGLLDQrlALkVWqdNIaaFGGDPnsVTifGe
 G++GFLst+d+++ GN+GLLDQ +AL+WVq+NIAaFGGDP++VT+FG+
 18903 196 GIFGFLSTDDSHAR--GNWGLLDQMAALRWVQENIAAFGGDPGNVTILFGQ 243

 SAGaaSVsl1111sngGDNppsskgLFhRAIsqSGsalspwaIQsesnarg
 SAGa+S+s l++s p++ GLFhRAIsqSG+al +i+s+ +
 18903 244 SAGAMSISGLMMS-----ELA-SGLFhRAIsqSGTALFRLFITSNP--LK 285

 rakelarllGCnetssellldClRksaaeeLleatrsfllfeyvpflplf
 ak++a l+GCn++s l+ CLR s + + + + + f + + f +
 18903 286 VAKKVAHLAGCNHNSTQILVNCIRALSGTKVMRVSNK-MRFLQLNFQ RDP 334

 l....aFgPvvDGdDapeafipEdPeelikeGkfadvPyliGvtkdEGgy
 ++ + +PvvDG+ +ip+dP+ l+ +Gk + vPyl Gv++ E+ +
 18903 335 EeiiwSMSPVVDGV-----VIPDDPLVLLTQGVSSVPYLLGVNNLEFNW 379

 faamlInasskgedelkktndpvdwlellkyllyfayasealnikdMddlad
 +++ + + + + ket ++ l+ ll+ + +
 18903 380 LLPYIMKFFPLNR-QAMRKETITK-MLWSTRTLLN-ITKEQ-----VP 418

 kvlekYpgdvddfsvesrknqlqdmldl1FkcptrvaadlhakhggsPv
 v e+Y++ v + + ++ + d++ D +F+++ + ++ ++++g Pv
 18903 419 LVVEEYLDNVNEHDWKMLNRMMDIVQDATEFVYA-TLQTAHYHRDAGLPV 467

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FIG. 3C

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18903 468 YaYvfdhpsfgigQflakrvdpefggavHgdeIffvFgnplllkeqlyka
Y+Y+f h+a+ + v+p+++ga+Hgde++f+Fg p+ ++ l
YLYEFEHHAR-----GIIVKPRTDGADHGDEMYFLFGGPFATG-LS-- 507

teeeeksssktmmnywanFAktGnPnnngtsnglvvWpkytseeqYslli
e++ts +mm+yywanFA+tGnP n++ +l+ Wp y+++e +l+
18903 508 MGKEKALS-LQMMKYWANFARTGNP-NDG--NLPCWPRYNKDEK--YLQL 551

llttitaqklkardprkvlcnfw<-*
+tt +klk+++ ++fw
18903 552 DFTTRVGMKLKEKK-----MAFW 569

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Searching for complete domains in SMART

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FIG. 4A

GAP of: FrGcgManager_76_IOA81nWg_ check: 5132 from: 1 to: 1983

Fbh18903FL - Import - vector trimmed

to: FrGcgManager_76_JOA3WXZ1_ check: 1319 from: 1 to: 2456

z34105 in Patent Nucleotide

Symbol comparison table: /ddm_local/gcg/gcg_9.1/

1/gcgcore/data/rundata/nwsgapdna.cmp

CompCheck: 8760

Gap Weight:	12	Average Match:	10.000
Length Weight:	4	Average Mismatch:	0.000

Quality:	13796	Length:	2746
Ratio:	6.957	Gaps:	14
Percent Similarity:	92.617	Percent Identity:	92.617

Match display thresholds for the alignment(s):

| = IDENTITY
: = 5
. = 1

FrGcgManager_76_IOA81nWg_ x FrGcgManager_76_JOA3WXZ1

..

```
COE-2      1 .....CCT 3
Z34105 101 CATTTGCGCCTTGCTGACGGCGTCGAGCCCTGGCCAGACATGTCCACAGGG 150
          4 TTAGCCAATTCGGCCGAGGCCTCCCGCCCCAGTA.CTTGCTGGCAGGGAT 52
          || || | || | | | | | | | | | | | | | | | | | | | | |
151 TTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACCGTGGCCGCGGCGG 200
          53 TAAGAGCAGA.TAAAAGTGTGCTCACACACTGTAGACACGGCTACCATGC 101
          | |||| | | | | | | | | | | | | | | | | | | | | | |
201 GACCAGCACAGGCGGCGTTTTCTCCTTCGGAACGGGAACGTCTAGCAACC 250
          102 CATC.....CACAGTGTGCCATCCACAGTGTGCCATCACTCCTGC. 143
          | || | | | | | | | | | | | | | | | | | | | | | | |
251 CTTCTGTGGGGCTCAATTTTGGAATCTTGGAAGTACTTCAACTCCAGCA 300
          144 .CCACAGCAGGAGCT..GGCTGGAGCATGAGGTGGATTCTGTG..CTGGA 188
          | |||| | | | | | | | | | | | | | | | | | | | | | |
301 ACTACATCTGCTCCTTCAAGTGTTTTTGGAACCGGGCTCTTTGGATCTAA 350
```


[illegible]

189 GCCTCACCCCT...CTGCCTGATGGCGCAGACGGCCTTGGGTGCCTTGCAC 235
||| | || | || | | | | |||||||||

351 ACCTGCCACTGGGTTCCTCTAGGAGGA.ACAAATACAGGTGCCTTGCAC 399

236 ACCAAGAGGCCTCAAGTGGTCACCAAATATGGAACCCTGCAAGGAAAACA 285
||||||||||||||||||||||||||||||||||||||||||||||||||

400 ACCAAGAGGCCTCAAGTGGTCACCAAATATGGAACCCTGCAAGGAAAACA 449

286 GATGCATGTGGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCCTTCT 335
||||||||||||||||||||||||||||||||||||||||||||||||||

450 GATGCATGTGGGGAAGACACCCATCCAAGTCTTTTTAGGAGTCCCCTTCT 499

336 CCAGACCTCCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCCGGAG 385
||||||||||||||||||||||||||||||||||||||||||||||||||

500 CCAGACCTCCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCCGGAG 549

386 CCCTGGAAAGGAATCAGAGATGCTACCACCTACCCGCCTG..... 425
||||||||||||||||||||||||||||||||||||||||||

550 CCCTGGAAAGGAATCAGAGATGCTACCACCTACCCGCCTGGATGGAGTCT 599

.

.

.

426GGTGCCTGCAGGAGTCCTGGGGCCAGCTGGCCTCGATGTA 465
||||||||||||||||||||||||||||||||||||||||||||||||||

700 TGGGGCTACAGGTGCCTGCAGGAGTCCTGGGGCCAGCTGGCCTCGATGTA 749

466 CGTCAGCACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTC 515
||||||||||||||||||||||||||||||||||||||||||||||||||

750 CGTCAGCACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTC 799

516 TGTACCTGAACGTGTACGCGCCGGCGCGCGCCCGGGGATCCCCAGCTG 565
||||||||||||||||||||||||||||||||||||||||||||||||||

800 TGTACCTGAACGTGTACGCGCCGGCGCGCGCGCCCGGGGATCCCCAGCTG 849

566 CCAGTGATGGTCTGGTTCCCGGGAGGCGCCTTCATCGTGGGCGCTGCTTC 615
||||||||||||||||||||||||||||||||||||||||||||||||||

850 CCAGTGATGGTCTGGTTCCCGGGAGGCGCCTTCATCGTGGGCGCTGCTTC 899

616 TTCGTACGAGGGCTCTGACTTGGCCGCCCGCGAGAAAGTGGTGCTGGTGT 665
||||||||||||||||||||||||||||||||||||||||||||||||||

900 TTCGTACGAGGGCTCTGACTTGGCCGCCCGCGAGAAAGTGGTGCTGGTGT 949

666 TTCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGCACGGACGACAGC 715
||||||||||||||||||||||||||||||||||||||||||||||||||

950 TTCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGCACGGACGACAGC 999

716 CACGCGCGCGGGAAC TGGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTG 765

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FIG. 4C

766 GGTGCAGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCC 815
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 1050 GGTGCAGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCC 1099
 816 TGTTCGGCCAGTCGGCGGGGGGCCATGAGCATCTCAGGACTGATGATGTCA 865
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 1100 TGTTCGGCCAGTCGGCGGGGGGCCATGAGCATCTCAGGACTGATGATGTCA 1149
 866 CCCCTAGCCTCGGGTCTCTTCCATCGGGCCATTTCCCAGAGTGGCACCGC 915
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 1150 CCCCTAGCCTCGGGTCTCTTCCATCGGGCCATTTCCCAGAGTGGCACCGC 1199
 916 GTTATTCAGACTTTTTCATCACTAGTAACCCACTGAAAGTGGCCAAGAAGG 965
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 1200 GTTATTCAGACTTTTTCATCACTAGTAACCCACTGAAAGTGGCCAAGAAGG 1249
 966 TTGCCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAAC 1015
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 1250 TTGCCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAAC 1299
 1016 TGCCTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGAT 1065
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 1300 TGCCTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGAT 1349
 1066 GAGATTCCTCCAACCTGAACTTCCAGAGAGACCCGGAAGAGATTATCTGGT 1115
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 1350 GAGATTCCTCCAACCTGAACTTCCAGAGAGACCCGGAAGAGATTATCTGGT 1399
 1116 CCATGAGCCCTGTGGTGGATGGTGTGGTGGATCCCAGATGACCCTTTGGTG 1165
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 1400 CCATGAGCCCTGTGGTGGATGGTGTGGTGGATCCCAGATGACCCTTTGGTG 1449
 1166 CTCCTGACCCAGGGGAAGGTTTTCATCTGTGCCCTACCTTCTAGGTGTCAA 1215
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 1450 CTCCTGACCCAGGGGAAGGTTTTCATCTGTGCCCTACCTTCTAGGTGTCAA 1499
 1216 CAACCTGGAATTCAATTGGCTCTTGCCTTATATCATGAAGTTCCCGCTAA 1265
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 1500 CAACCTGGAATTCAATTGGCTCTTGCCTTAT..... 1530
 .
 .
 .
 1316 CGCACCCCTGTTGAATATACCAAGGAGCAGGTACCACTTGTGGTGGAGGA 1365
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 1531AATATACCAAGGAGCAGGTACCACTTGTGGTGGAGGA 1568
 1366 GTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAAACCGTA 1415

ccttgcaggaattcaattggctcttgccttata

FIG. 4D

1416	TGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCACACTGCAGACT	1465
1619	TGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCACACTGCAGACT	1668
1466	GCTCACTACCACCGAGATGCCGGCCTCCCTGTCTACCTGTATGAATTTGA	1515
1669	GCTCACTACCACCGA.....	1683
	
	
1666	CAACTTTGCCCGCACAGGAAACCCCAATGATGGGAATCTGCCCTGCTGGC	1715
1684GAAACCCCAATGATGGGAATCTGCCCTGCTGGC	1716
	
1716	CACGCTACAACAAGGATGAAAAGTACCTGCAGCTGGATTTTACCACAAGA	1765
1717	CACGCTACAACAAGGATGAAAAGTACCTGCAGCTGGATTTTACCACAAGA	1766
1766	GTGGGCATGAAGCTCAAGGAGAAGAAGATGGCTTTTTTGATGAGTCTGTA	1815
1767	GTGGGCATGAAGCTCAAGGAGAAGAAGATGGCTTTTTTGATGAGTCTGTA	1816
1816	CCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGCTATGCA	1865
1817	CCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGCTATGCA	1866
1866	GGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGAC	1915
1867	GGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGAC	1916
1916	TAGCCATGGACATACCTGGGGACAAGAGTTCTACCCAAGGGCGAATTCGT	1965
1917	TAGCCATGGACATACCTGGGGACAAGAGTTCTACCCA...CCCCA...GT	1960
1966	TTAAACCTGCAGGA.CTAG.....	1983
1961	TTAGAACTGCAGGAGCTCCCTGCTGCCTCCAGGCCAAAGCTAGAGCTTTT	2010

FIG. 5A

ALIGN calculates a global alignment of two sequences
version 2.0uPlease cite: Myers and Miller, CABIOS (1989)

COE-2 584 aa vs.

PRO873 545 aa

scoring matrix: BLOSUM50, gap penalties: -12/-2

62.4% identity; Global alignment score: 2271

```

COE-2  M-----PST-----VLPSTVLPSSLPTAG
      :
pro873 MSTGFSFGSGTLGSTTTVAAGTSTGGVFSFGTGTSSNPSSVGLNFGNLGSTSTPATTSAPS
      10  20  30  40  50  60
      20  30  40  50  60
COE-2  AGWSMRWILCWSLTLCLMAQTALGALHTKRPQVVTKYGTIQGKQMHVGTKPIQVFLGVPF
      :
pro873 SGFGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTIQGKQMHVGTKPIQVFLGVPF
      70  80  90  100  110  120
      80  90  100  110
COE-2  SRPPLGILRFAPPEPPEPWKGIRDATTYPG-----
      :
pro873 SRPPLGILRFAPPEPPEPWKGIRDATTYPPGWSLALSPGWSAVARSRLTATSASRVQASL
      130  140  150  160  170  180
      120  130  140  150
COE-2  -----CLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVAAPARAPGDPQLPVM
      :
pro873 LPQPLSVWGYRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVAAPARAPGDPQLPVM
      190  200  210  220  230  240

```

FIG. 5B

	160	170	180	190	200	210
COE-2	VFPPGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGLSTDDSHARGNWGLLDQMA					

ppro873	VFPPGAFIVGAASSYEGSDLAAREKVVLVFLQHRLGIFGLSTDDSHARGNWGLLDQMA					
	250	260	270	280	290	300

	220	230	240	250	260	270
COE-2	ALRWQENIAAFGGDPGNVTLFGQSAGAMISGLMMSPLASGLFHRAISQSGTALFRLFI					
	::					
pro873	ALRWQENIAAFGGDPGNVTLFGQSAGAMISGLMMSPLASGLFHRAISQSGTALFRLFI					
	310	320	330	340	350	360

	280	290	300	310	320	330
COE-2	TSNPLKVAKKV	AHLACGNHNS	TQILVNCLRALSGTKVMRVS	NKMRFQLNFQRDPEETIIW ::: :::		
pro873	TSNPLKVAKKV	AHLACGNHNS	TQILVNCLRALSGTKVMRVS	NKMRFQLNFQRDPEETIIW ::: :::		
	370	380	390	400	410	420

[illegible]

	400	410	420	430	440	450
COE-2	TKMLWSTRLLNITKEQVPLVVEEYLDNVNEHDWKMLRNRMDIVQDATFVYATLQTAHY					
pro873	-----NITKEQVPLVVEEYLDNVNEHDWKMLRNRMDIVQDATFVYATLQTAHY					

FIG. 5C

```

460      470      480      490      500      510
COE-2  HRDAGLPVLYEFEEHHARGIIVKPRTDGADHGDEMYFLFGGPFATGLSMGKEKALSLOMM
      :... :... :... :... :... :...
pro873 HRET--PMM-----GIC--P-----AGHA-----
      520

520      530      540      550      560      570
COE-2  KYWANFARTGNPNDGNLPCWPRYNKDEKYLQDFTTRVGMKLEKEMAFWMSLYQSORPE
      :... :... :... :... :... :...
pro873 -----TTRM-----KSTCSWIL-----P-
      530      540

580
COE-2  KQRQF
      :...
pro873 -QEWA

```

FIG. 6A

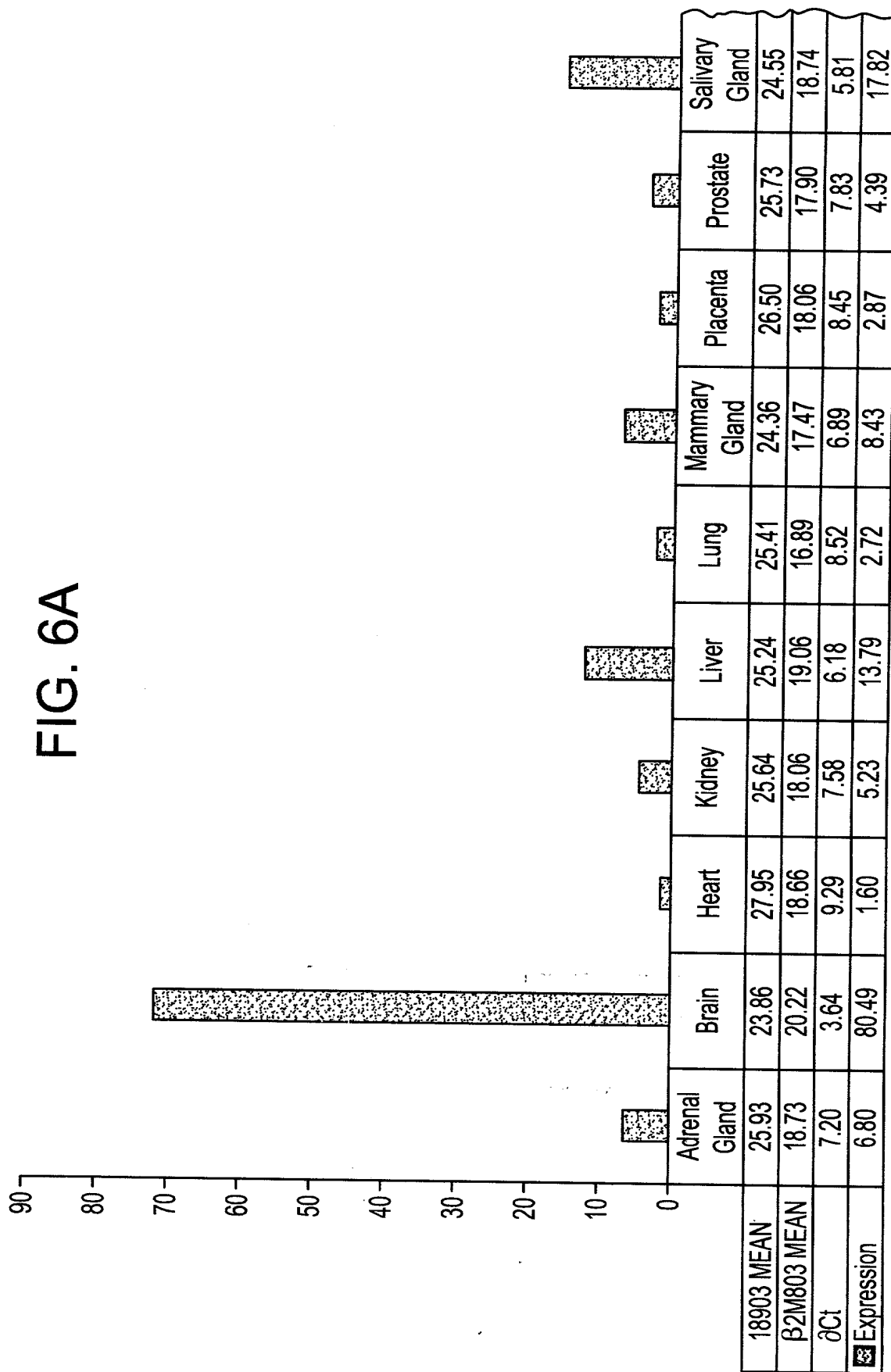


FIG. 6B

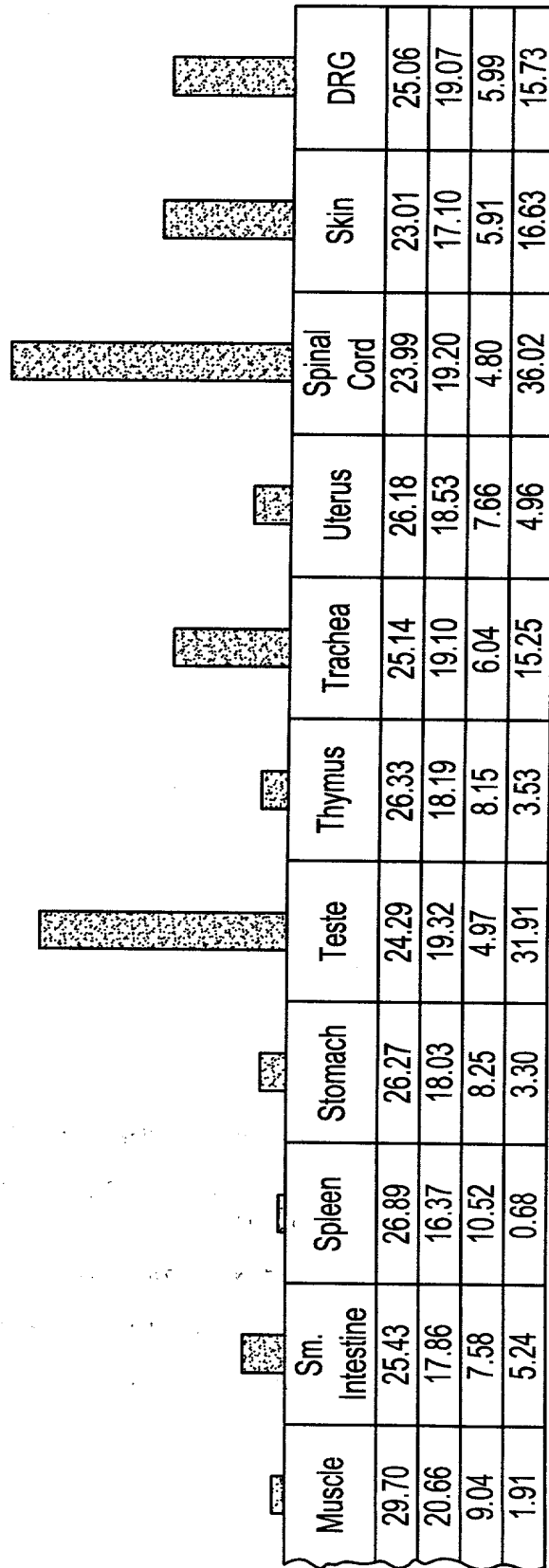


FIG. 7A

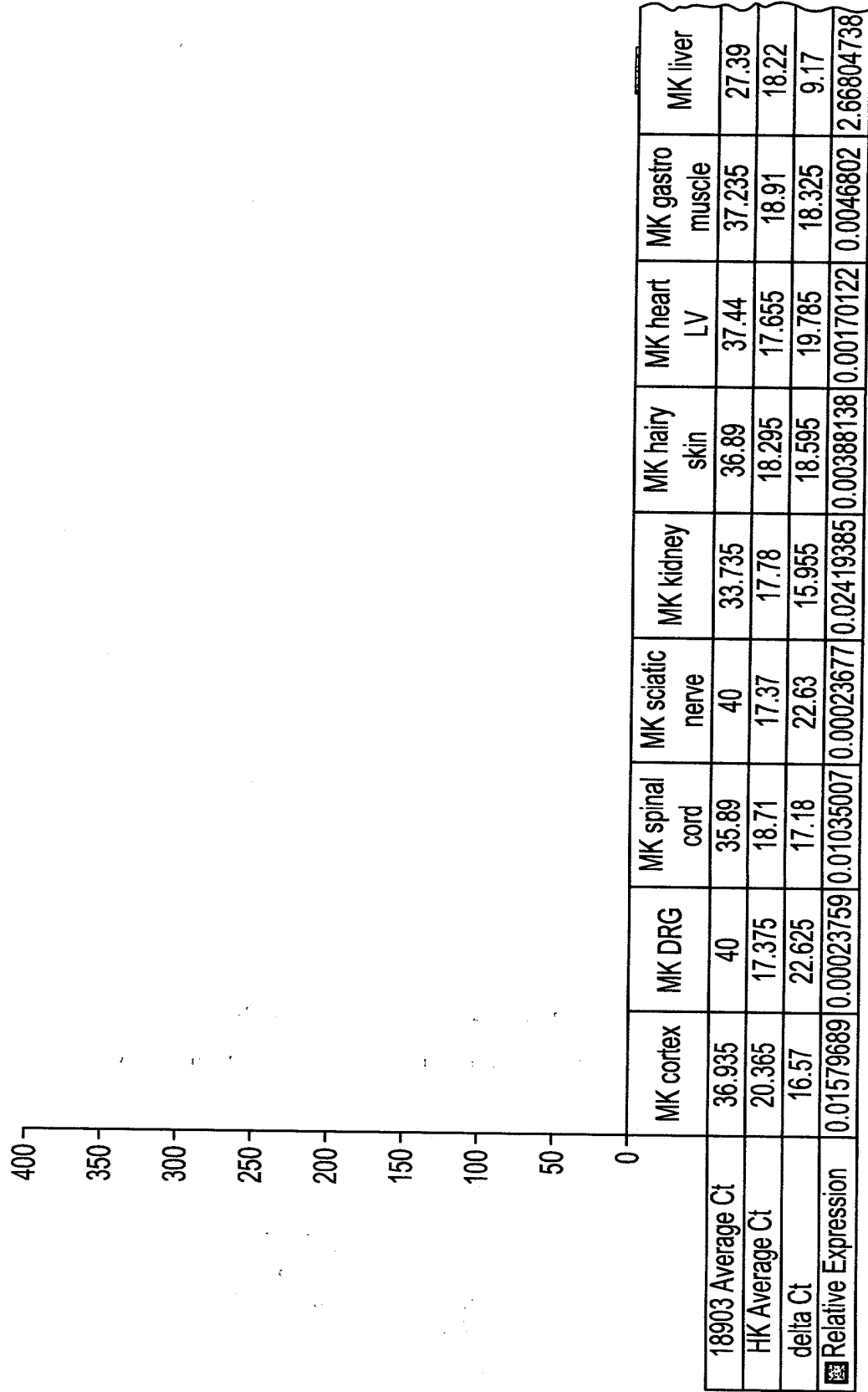


FIG. 7B

Hu. Brain	Hu. Spinal cord	Hu. Heart	Hu. Kidney	Hu. Liver	Hu. Lung
21.27	23.78	28.26	26.155	25.43	25.805
19.245	18.295	17.855	17.925	18.22	15.87
2.025	5.485	10.405	8.23	7.21	9.935
377.618146	34.3154004	1.13349992	5.11872423	10.3803579	1.57002147

FIG. 8A-1

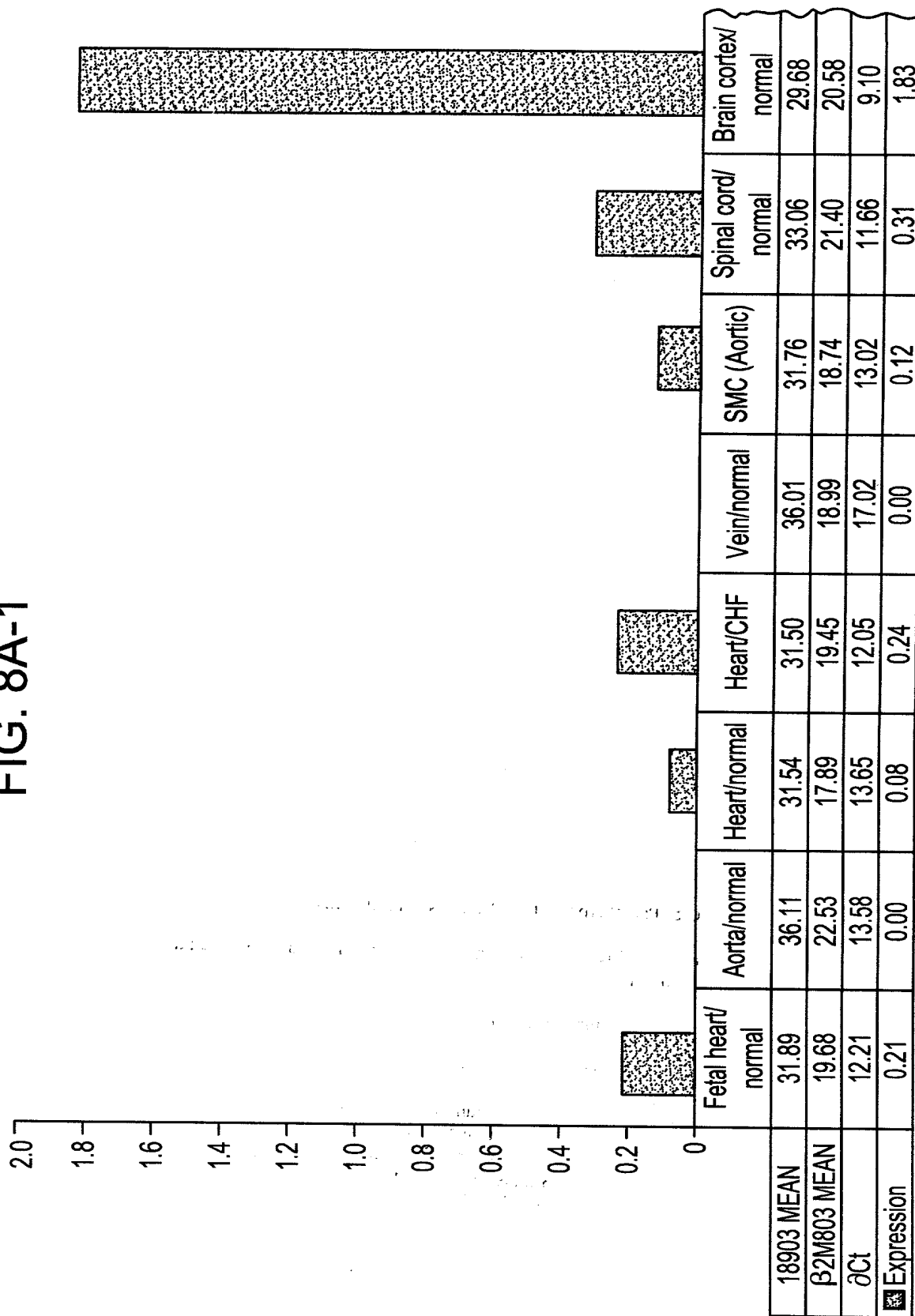
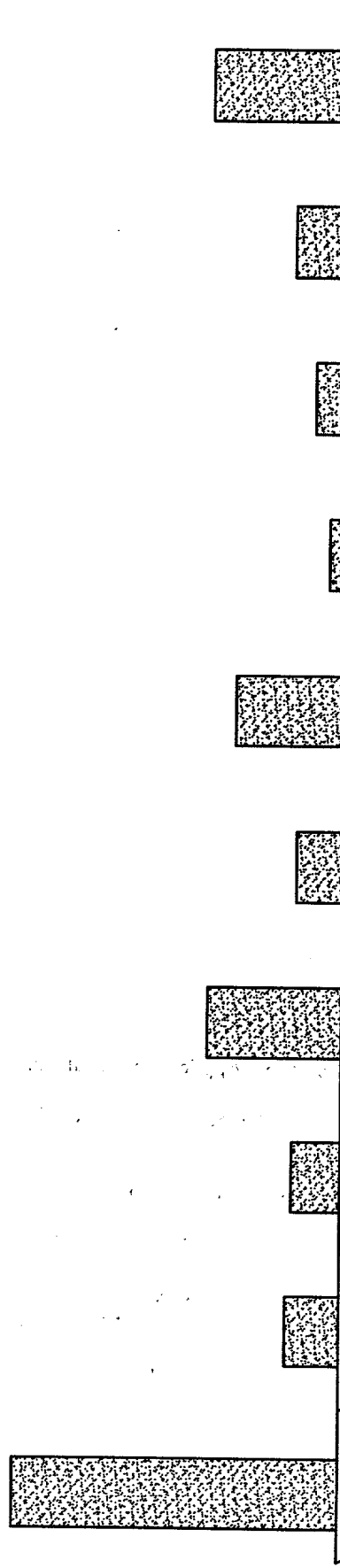
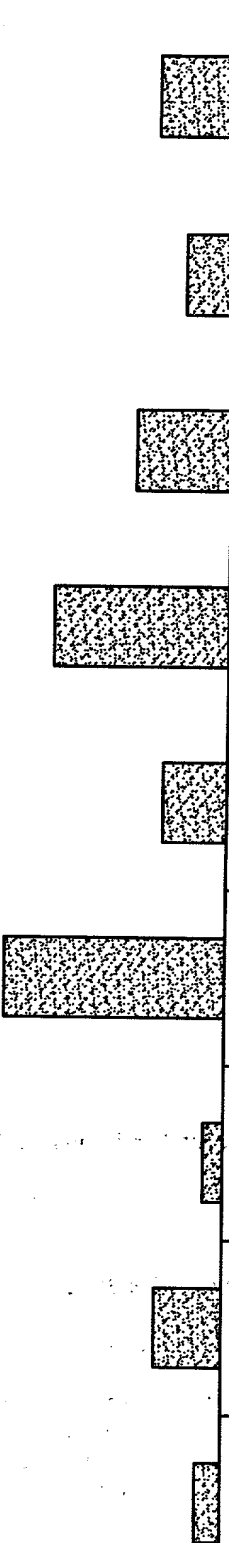


FIG. 8A-2



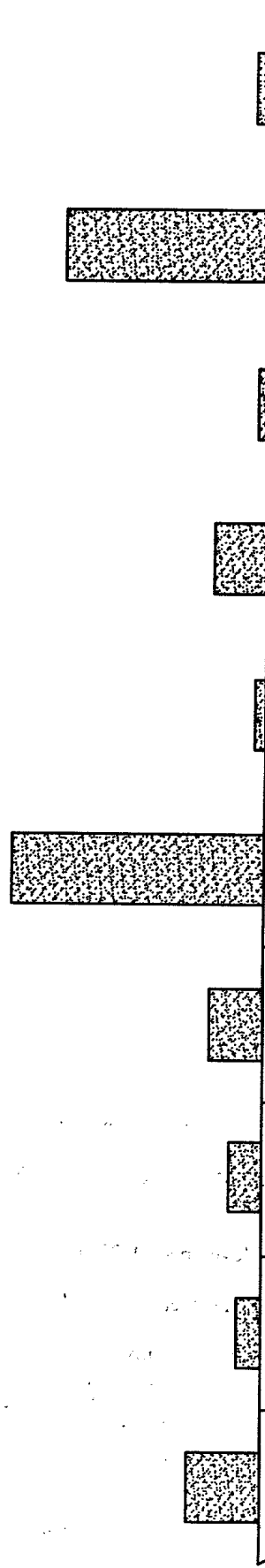
	Brain hypothalamus	Glia cells (Astrocytes)	Brain/ Glioblastoma	Breast/ normal	Breast tumor/ IDC	OVARY/ Normal	OVARY/ Tumor	Pancreas	Prostate/ Normal	Prostate/ Tumor
	29.45	33.94	30.39	30.10	30.75	31.73	33.59	30.88	31.16	29.03
	19.24	21.09	17.43	18.60	17.66	19.95	18.91	17.33	18.34	17.57
	10.21	12.86	12.97	11.50	13.09	11.79	14.68	13.55	12.83	11.46
	0.85	0.13	0.13	0.35	0.11	0.28	0.04	0.08	0.14	0.35

FIG. 8A-3



Colon/normal	Colon/tumor	Colon/IBD	Kidney/normal	Liver/normal	Liver fibrosis	Fetal Liver/normal	Lung/normal	Lung/tumor
32.03	30.80	32.37	30.98	31.82	30.10	33.55	30.54	30.30
17.78	18.15	17.72	20.03	19.08	18.82	21.39	17.31	17.77
14.26	12.66	14.65	10.95	12.75	11.29	12.16	13.23	12.53
0.05	0.16	0.04	0.51	0.15	0.40	0.22	0.10	0.17

FIG. 8A-4



Lung/COPD	Tonsil/normal	Lymph node/normal	Thymus/normal	Epithelial Cells (Prostate)	Endothelial Cells (Aortic)	Skeletal Muscle	Fibroblasts (Dermal)	Skin/Normal	Adipose/Normal
29.44	31.13	31.40	32.80	30.70	35.27	31.06	33.10	31.16	32.43
17.10	17.19	17.91	20.03	20.13	20.16	18.26	18.18	20.29	17.96
12.34	13.94	13.49	12.78	10.57	15.11	12.81	14.92	10.87	14.47
0.19	0.06	0.09	0.14	0.66	0.03	0.14	0.03	0.54	0.04

FIG. 8A-5

Osteoblasts (Primary)	Osteoblasts (Undiff)	Osteoblasts (Diff)	Osteoclasts	Aorta SMC (Early)	Aorta SMC (Late)	HUVEC	HMVEC
34.84	33.19	33.23	32.47	32.50	32.72	32.17	32.74
20.44	18.50	17.83	17.25	19.53	18.77	19.27	18.74
14.40	14.69	15.40	15.22	12.97	13.96	12.91	14.00
0.05	0.04	0.02	0.03	0.13	0.06	0.13	0.06

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FIG. 8B

Tissue	18903 MEAN	β 2M803 MEAN	δ Ct	Expression
Fetal heart/normal	31.89	19.68	12.21	0.21
Aorta/normal	36.11	22.53	13.58	0.00
Heart normal	31.54	17.89	13.65	0.08
Heart/CHF	31.50	19.45	12.05	0.24
Vein/normal	36.01	18.99	17.02	0.00
SMC (Aortic)	31.76	18.74	13.02	0.12
Spinal cord/normal	33.06	21.40	11.66	0.31
Brain cortex/normal	29.68	20.58	9.10	1.83
Brain hypothalamus/normal	29.45	19.24	10.21	0.85
Glial cells (Astrocytes)	33.94	21.09	12.86	0.13
Brain/Glioblastoma	30.39	17.43	12.97	0.13
Breast/normal	30.10	18.60	11.50	0.35
Breast tumor/IDC	30.75	17.66	13.09	0.11
Ovary/normal	31.73	19.95	11.79	0.28
Ovary/tumor	33.59	18.91	14.68	0.04
Pancreas	30.88	17.33	13.55	0.08
Prostate/normal	31.16	18.34	12.83	0.14
Prostate/tumor	29.03	17.57	11.46	0.35
Colon/normal	32.03	17.78	14.26	0.05
Colon/tumor	30.80	18.15	12.66	0.16
Colon/IBD	32.37	17.72	14.65	0.04
Kidney/normal	30.98	20.03	10.95	0.51
Liver/normal	31.82	19.08	12.75	0.15
Liver/fibrosis	30.10	18.82	11.29	0.40
Fetal Liver/normal	33.55	21.39	12.16	0.22
Lung/normal	30.54	17.31	13.23	0.10
Lung/tumor	30.30	17.77	12.53	0.17
Lung/COPD	29.44	17.10	12.34	0.19
Tonsil/normal	31.13	17.19	13.94	0.06
Lymph node/normal	31.40	17.91	13.49	0.09
Thymus/normal	32.80	20.03	12.78	0.14
Epithelial Cells(prostate)	30.70	20.13	10.57	0.66
Endothelial Cells(aortic)	35.27	20.16	15.11	0.03
Skeletal Muscle/normal	31.06	18.26	12.81	0.14
Fibroblasts (Dermal)	33.10	18.18	14.92	0.03
Skin/normal	31.16	20.29	10.87	0.54
Adipose/normal	32.43	17.96	14.47	0.04
Osteoblasts (primary)	34.84	20.44	14.40	0.05
Osteoblasts (Undiff)	33.19	18.50	14.69	0.04
Osteoblasts (Diff)	33.23	17.83	15.40	0.02
Osteoblasts	32.47	17.25	15.22	0.03
Aorta SMC (Early)	32.50	19.53	12.97	0.13
Aorta SMC (Late)	32.72	18.77	13.96	0.06
HUVEC	32.17	19.27	12.91	0.13
HMVEC	32.74	18.74	14.00	0.06
	40.00	40.00	0.00	